

SubstCRFsequencelisting_2009Ju130.txt

SEQUENCE LISTING

<110> KIM, Young Tae
LEE, Jae Hyung

<120> Gene involved in the biosynthesis of carotenoid and marine microorganism, paracoccus haeundaeensis, producing the carotenoid

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<140> US 10/551,508
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<151> 2003-03-31

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Leu Asp His Ala Ala Gly Pro Ser Asp Gly His Thr Trp Ser Cys His
35 40 45

Asp Pro Asp Leu Ser Pro His Trp Leu Ala Arg Leu Lys Pro Leu Arg
50 55 60

Arg Ala Asn Trp Pro Asp Gln Glu Val Arg Phe Pro Arg His Ala Arg
65 70 75 80

SubstCRFsequencelisting_2009Jul30.txt

Arg Leu Ala Thr Gly Tyr Gly Ser Leu Asp Gly Ala Ala Leu Ala Asp
85 90 95

Ala Val Ala Arg Ser Gly Ala Glu Ile Arg Trp Asn Ser Asp Ile Ala
100 105 110

Leu Leu Asp Glu Gln Gly Ala Thr Leu Ser Cys Gly Thr Arg Ile Glu
115 120 125

Ala Gly Ala Val Leu Asp Gly Arg Gly Ala Gln Pro Ser Arg His Leu
130 135 140

Thr Val Gly Phe Gln Lys Phe Val Gly Val Glu Ile Glu Thr Asp Cys
145 150 155 160

Pro His Gly Val Pro Arg Pro Met Ile Met Asp Ala Thr Val Thr Gln
165 170 175

Gln Asp Gly Tyr Arg Phe Ile Tyr Leu Leu Pro Phe Ser Pro Thr Arg
180 185 190

Ile Leu Ile Glu Asp Thr Arg Tyr Ser Asp Gly Gly Asn Leu Asp Asp
195 200 205

Asp Ala Leu Ala Ala Ala Ser His Asp Tyr Ala Arg Gln Gln Gly Trp
210 215 220

Thr Gly Ala Glu Val Arg Arg Glu Arg Gly Ile Leu Pro Ile Ala Leu
225 230 235 240

Ala His Asp Ala Ala Gly Phe Trp Ala Asp His Ala Glu Gly Pro Val
245 250 255

Pro Val Gly Leu Arg Ala Gly Phe Phe His Pro Val Thr Gly Tyr Ser
260 265 270

Leu Pro Tyr Ala Ala Gln Val Ala Asp Val Val Ala Gly Leu Ser Gly
275 280 285

Pro Pro Gly Thr Asp Ala Leu Arg Gly Ala Ile Arg Asp Tyr Ala Ile
290 295 300

Asp Arg Ala Arg Arg Asp Arg Phe Leu Arg Leu Leu Asn Arg Met Leu
305 310 315 320

Phe Arg Gly Cys Ala Pro Asp Arg Arg Tyr Thr Leu Leu Gln Arg Phe
325 330 335

Tyr Arg Met Pro His Gly Leu Ile Glu Arg Phe Tyr Ala Gly Arg Leu
340 345 350

Ser Val Ala Asp Gln Leu Arg Ile Val Thr Gly Lys Pro Pro Ile Pro
355 360 365

Leu Gly Thr Ala Ile Arg Cys Leu Pro Glu Arg Pro Leu Leu Lys Glu
370 375 380

Asn Ala
385

SubstCRFsequencelisting_2009Jul30.txt

<211> 1506

<212> DNA

<213> Paracoccus haeundaeensis

<220>

<223> crtI gene

<400> 11

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ctggccctgg	ccatccgcct	gcagtccgcg	ggcatcgcca	ccaccctgg	cgaggcccg	120
gacaagcccg	gcgggcgcgc	ctatgtctgg	cacgatcagg	gccatgttct	cgacgcgggc	180
ccgaccgtca	tcaccgaccc	cgatgcgc	aaggagctgt	gggcgtgac	cggcaggac	240
atggcgcgcg	acgtgacgct	gatgccgg	tgc	atcgactgat	gtggccggc	300
ggaaaggtct	tcgattacgt	gaacgaggcc	gatcagctgg	agcgccagat	cgc	360
aacccggacg	accttggagg	ataccgcgc	ttccgtgatt	acgcggagga	gtgtatcag	420
gagggctacg	tcaagctgg	caccgtgccc	ttcctcaagc	tggccagat	gctcaaggcc	480
gcgc	cg	tgatgaagct	ggaggcctat	aagtccgtcc	atgccaaggt	540
atcaaggacc	cctatctgcg	gcaggcg	ttt	tcgtatcaca	cgctgtgg	600
cccttctga	ccagctcgat	ctatgcgt	atccacgcgc	tggagcgg	cggcggg	660
tgg	tc	aggcggcac	caaccagctg	gtcg	gttcaacgg	720
cttggcggcc	agatgtat	gaacgccaag	gtcg	tgcagaccga	ggcgcgc	780
accacggcgc	tcaccctggc	ggacggcgg	tctttaaggg	ccgacatgg	cgc	840
ggcgcacgtca	tgcacaacta	tcgcgac	ctgg	ccaca	cgcccgc	900
gcgaaatcgc	tggaccgcaa	gcgcgtgt	atgtcg	tgc	gttcaacgg	960
cgcgaggcgc	ccaaggacat	cg	ccatcctgt	tcgg	ccatcaggag	1020
ctgg	tc	atcgat	ctgg	tcgt	tttcgg	1080
tcgc	ccatctgg	ggacatggc	cctccgg	tgtccacg	ttacgt	1140
gccccgtgc	cgatctgg	ccgcgc	atcgat	cggtcg	gttcaacgg	1200
gccgaccgc	tcctggcgt	cctggagg	cggtgat	ccaaac	cgccaa	1260
accacgacgc	gcatttcac	gccgcgc	ttcgcc	ctgc	ccatcacggc	1320
agcgc	tttct	cgatggcc	gatcctg	caatccgc	aa	1380
gacaagacga	tccgcaactt	ctatctgg	ggcgcgg	ccc	tttccgg	1440
ccggcgtcg	tgg	ctggcggc	caaggccacg	ccc	cgcccagg	1500
gcatga						1506

<210> 12

<211> 501

SubstCRFsequencelisting_2009Jul30.txt

<212> PRT

<213> Paracoccus haeundaeensis

<220>

<223> crtI amino acid

<400> 12

Met Asn Ala His Ser Pro Ala Ala Lys Thr Ala Ile Val Ile Gly Ala
1 5 10 15

Gly Phe Gly Gly Leu Ala Leu Ala Ile Arg Leu Gln Ser Ala Gly Ile
20 25 30

Ala Thr Thr Leu Val Glu Ala Arg Asp Lys Pro Gly Gly Arg Ala Tyr
35 40 45

Val Trp His Asp Gln Gly His Val Phe Asp Ala Gly Pro Thr Val Ile
50 55 60

Thr Asp Pro Asp Ala Leu Lys Glu Leu Trp Ala Leu Thr Gly Gln Asp
65 70 75 80

Met Ala Arg Asp Val Thr Leu Met Pro Val Ser Pro Phe Tyr Arg Leu
85 90 95

Met Trp Pro Gly Gly Lys Val Phe Asp Tyr Val Asn Glu Ala Asp Gln
100 105 110

Leu Glu Arg Gln Ile Ala Gln Phe Asn Pro Asp Asp Leu Glu Gly Tyr
115 120 125

Arg Arg Phe Arg Asp Tyr Ala Glu Glu Val Tyr Gln Glu Gly Tyr Val
130 135 140

Lys Leu Gly Thr Val Pro Phe Leu Lys Leu Gly Gln Met Leu Lys Ala
145 150 155 160

Ala Pro Ala Leu Met Lys Leu Glu Ala Tyr Lys Ser Val His Ala Lys
165 170 175

Val Ala Thr Phe Ile Lys Asp Pro Tyr Leu Arg Gln Ala Phe Ser Tyr
180 185 190

His Thr Leu Leu Val Gly Gln Asn Pro Phe Ser Thr Ser Ser Ile Tyr
195 200 205

Ala Leu Ile His Ala Leu Glu Arg Arg Gly Val Trp Phe Ala Lys
210 215 220

Gly Gly Thr Asn Gln Leu Val Ala Gly Met Val Ala Leu Phe Glu Arg
225 230 235 240

Leu Gly Gly Gln Met Met Leu Asn Ala Lys Val Ala Arg Ile Glu Thr
245 250 255

Glu Gly Ala Arg Thr Thr Gly Val Thr Leu Ala Asp Gly Arg Ser Leu
260 265 270

Arg Ala Asp Met Val Ala Ser Asn Gly Asp Val Met His Asn Tyr Arg
275 280 285

Asp Leu Leu Gly His Thr Ala Arg Gly Gln Ser Arg Ala Lys Ser Leu
290 295 300

SubstCRFsequencelisting_2009Jul30.txt

Asp Arg Lys Arg Trp Ser Met Ser Leu Phe Val Leu His Phe Gly Leu
305 310 315 320

Arg Glu Ala Pro Lys Asp Ile Ala His His Thr Ile Leu Phe Gly Pro
325 330 335

Arg Tyr Arg Glu Leu Val Asn Glu Ile Phe Lys Gly Pro Lys Leu Ala
340 345 350

Glu Asp Phe Ser Leu Tyr Leu His Ser Pro Cys Thr Thr Asp Pro Asp
355 360 365

Met Ala Pro Pro Gly Met Ser Thr His Tyr Val Leu Ala Pro Val Pro
370 375 380

His Leu Gly Arg Ala Glu Ile Asp Trp Ala Val Glu Gly Pro Arg Tyr
385 390 395 400

Ala Asp Arg Ile Leu Ala Ser Leu Glu Glu Arg Leu Ile Pro Asn Leu
405 410 415

Arg Ala Asn Leu Thr Thr Arg Ile Phe Thr Pro Ala Asp Phe Ala
420 425 430

Ser Glu Leu Asn Ala His His Gly Ser Ala Phe Ser Val Glu Pro Ile
435 440 445

Leu Thr Gln Ser Ala Trp Phe Arg Pro His Asn Arg Asp Lys Thr Ile
450 455 460

Arg Asn Phe Tyr Leu Val Gly Ala Gly Thr His Pro Gly Ala Gly Ile
465 470 475 480

Pro Gly Val Val Gly Ser Ala Lys Ala Thr Ala Gln Val Met Leu Ser
485 490 495

Asp Leu Ala Gly Ala
500

<210> 13
<211> 915
<212> DNA
<213> Paracoccus haeundaeensis

* <220>
<223> crtB gene

<400> 13
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acggcggcca agctgatgcc gccgggcattc cgcgacgaca cggtgatgct ctatgcctgg 120
tgccgccacg cggatgacgt gatcgacggt caggccctgg gcagccgccc cgaggcggtg 180
aacgacccgc aggcgccgct ggacggcctg cgctcgacca cgctggcggc cctgcaggc 240
gacggtccgg tgacccccgcc ctttgcgcgg ctgcgcgcgg tggcgcggcg gcatgatttc 300
ccgcaggcct ggcccatgga cctgatcgaa ggcttcgcga tggatgtcgaa ggcgccgac 360

SubstCRFsequencelisting_2009Jul30.txt

tatcgacgc	tggatgacgt	gctggatat	tcctatcacg	tcgcaggcat	cgtcgccgtg	420
atgatggccc	gcgtgatggg	cgtcgccgac	gatcctgtcc	tggaccgcgc	ctgcgacctg	480
gggctggcgt	tccagctgac	caacatcgcg	cgcgacgtga	tcgacgatgc	gcgcatcgaa	540
cggtgctatc	tgccggggga	ctggctggac	caggcgggcg	cgcggatcga	cgggccccgtg	600
ccgtcgccgg	agctgtacac	agtatcctc	cggctttgg	atgaggcgaa	accctattac	660
gcgtcgccgc	gggtgggtct	ggcggatctg	ccaccgcgt	gcgcctggtc	catcgccgcc	720
gcgcgtacgga	tctatcgccgc	catcggtctg	cgcacccgca	agagcgggccc	gcaggcctat	780
cgcacccgga	tcagcacgtc	caaggctgcc	aagatcgcc	tgctggcgt	cggggctgg	840
gatgtcgccgc	gatcacgcct	gccggggcgc	ggcgtgtcgc	ggcagggcct	ctggaccgg	900
ccgcacatcacg	tcttag					915

<210> 14
<211> 304
<212> PRT
<213> Paracoccus haeundaeensis

<220>
<223> crtB amino acid

<400> 14
Met Ser Asp Leu Val Leu Thr Ser Thr Glu Ala Ile Thr Gln Gly Ser
1 5 10 15

Gln Ser Phe Ala Thr Ala Ala Lys Leu Met Pro Pro Gly Ile Arg Asp
20 25 30

Asp Thr Val Met Leu Tyr Ala Trp Cys Arg His Ala Asp Asp Val Ile
35 40 45

Asp Gly Gln Ala Leu Gly Ser Arg Pro Glu Ala Val Asn Asp Pro Gln
50 55 60

Ala Arg Leu Asp Gly Leu Arg Val Asp Thr Leu Ala Ala Leu Gln Gly
65 70 75 80

Asp Gly Pro Val Thr Pro Pro Phe Ala Ala Leu Arg Ala Val Ala Arg
85 90 95

Arg His Asp Phe Pro Gln Ala Trp Pro Met Asp Leu Ile Glu Gly Phe
100 105 110

Ala Met Asp Val Glu Ala Arg Asp Tyr Arg Thr Leu Asp Asp Val Leu
115 120 125

Glu Tyr Ser Tyr His Val Ala Gly Ile Val Gly Val Met Met Ala Arg
130 135 140

Val Met Gly Val Arg Asp Asp Pro Val Leu Asp Arg Ala Cys Asp Leu
145 150 155 160

Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp Val Ile Asp Asp
165 170 175

SubstCRFsequencelisting_2009Jul30.txt

Ala Arg Ile Gly Arg Cys Tyr Leu Pro Gly Asp Trp Leu Asp Gln Ala
180 185 190

Gly Ala Arg Ile Asp Gly Pro Val Pro Ser Pro Glu Leu Tyr Thr Val
195 200 205

Ile Leu Arg Leu Leu Asp Glu Ala Glu Pro Tyr Tyr Ala Ser Ala Arg
210 215 220

Val Gly Leu Ala Asp Leu Pro Pro Arg Cys Ala Trp Ser Ile Ala Ala
225 230 235 240

Ala Leu Arg Ile Tyr Arg Ala Ile Gly Leu Arg Ile Arg Lys Ser Gly
245 250 255

Pro Gln Ala Tyr Arg Gln Arg Ile Ser Thr Ser Lys Ala Ala Lys Ile
260 265 270

Gly Leu Leu Gly Val Gly Gly Trp Asp Val Ala Arg Ser Arg Leu Pro
275 280 285

Gly Ala Gly Val Ser Arg Gln Gly Leu Trp Thr Arg Pro His His Val
290 295 300

<210> 15
<211> 882
<212> DNA
<213> Paracoccus haeundaeensis

<220>
<223> crtE gene

<400> 15
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gccccagggat tcggtgccgt gtcgcagccg ctcggcgccg ccatgagcca tggcgcgctg 120
tcgtcgggca ggcggttccg cggcatgctg atgctgcttgc cggcagaggc ctcgggcggg 180
gtctgcgaca cgatcgtcga cgcgcctgc gcggtcgaga tggtgcatgc cgcacatcgctg 240
atcttcgacg acctgcccctg catggacgat gccgggctgc gccgcggccg gcccgcgacc 300
catgtggcgc atggcgaaag ccgtgcccgtg ctggggcggca tcgcccgtat caccgaggca 360
atggccctgc tggccgggtgc gcgcggcgccg tcgggcacgg tgcgggcgca gctggtgccg 420
atcctgtcgc ggtccctggg gccgcaggccg ctgtgcgccc gccaggaccc ggacctgcac 480
gcggccaaga acggcgcggg ggtcgaacag gaacaggacc tgaagaccgg cgtgctgttc 540
atcgccgggc tggagatgtc ggcctgtatc aaggagttcg acgcccgggca gcagacccag 600
atgatcgact ttggccgtca gctgggcgcg gtgttccagt cctatgacga cctgctggac 660
gtcgtggcgc accaggcggc gcttggcaag gataccggc gcgatgccgc ggccccggc 720
ccgcggcgcc gccttctggc cgtgtcagac ctgcagaacg tgtccctgtca ttacgaggcc 780
agccgcgccc aactggacgc gatgctgcgc agcaagcgcc ttcaaggctcc ggaaatcgcg 840

SubstCRFsequencelisting_2009Jul30.txt

gccctgctgg aacgggttct gccctacgcc gcgcgcgcct ag

882

<210> 16
<211> 293
<212> PRT
<213> Paracoccus haeundaeensis

<220>
<223> crtE amino acid

<400> 16
Met Arg Arg Asp Val Asn Pro Ile His Ala Thr Leu Leu Gln Thr Arg
1 5 10 15
Leu Glu Glu Ile Ala Gln Gly Phe Gly Ala Val Ser Gln Pro Leu Gly
20 25 30
Ala Ala Met Ser His Gly Ala Leu Ser Ser Gly Arg Arg Phe Arg Gly
35 40 45
Met Leu Met Leu Leu Ala Ala Glu Ala Ser Gly Gly Val Cys Asp Thr
50 55 60
Ile Val Asp Ala Ala Cys Ala Val Glu Met Val His Ala Ala Ser Leu
65 70 75 80
Ile Phe Asp Asp Leu Pro Cys Met Asp Asp Ala Gly Leu Arg Arg Gly
85 90 95
Arg Pro Ala Thr His Val Ala His Gly Glu Ser Arg Ala Val Leu Gly
100 105 110
Gly Ile Ala Leu Ile Thr Glu Ala Met Ala Leu Leu Ala Gly Ala Arg
115 120 125
Gly Ala Ser Gly Thr Val Arg Ala Gln Leu Val Arg Ile Leu Ser Arg
130 135 140
Ser Leu Gly Pro Gln Gly Leu Cys Ala Gly Gln Asp Leu Asp Leu His
145 150 155 160
Ala Ala Lys Asn Gly Ala Gly Val Glu Gln Glu Gln Asp Leu Lys Thr
165 170 175
Gly Val Leu Phe Ile Ala Gly Leu Glu Met Leu Ala Val Ile Lys Glu
180 185 190
Phe Asp Ala Glu Glu Gln Thr Gln Met Ile Asp Phe Gly Arg Gln Leu
195 200 205
Gly Arg Val Phe Gln Ser Tyr Asp Asp Leu Leu Asp Val Val Gly Asp
210 215 220
Gln Ala Ala Leu Gly Lys Asp Thr Gly Arg Asp Ala Ala Ala Pro Gly
225 230 235 240
Pro Arg Arg Gly Leu Leu Ala Val Ser Asp Leu Gln Asn Val Ser Arg
245 250 255
His Tyr Glu Ala Ser Arg Ala Gln Leu Asp Ala Met Leu Arg Ser Lys
260 265 270

SubstCRFsequencelistings_2009Jul30.txt

Arg Leu Gln Ala Pro Glu Ile Ala Ala Leu Leu Glu Arg Val Leu Pro
275 280 285

Tyr Ala Ala Arg Ala
290

<210> 17
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for crt gene

<400> 17
gttccacgac tggggcatc 19

<210> 18
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for crt gene

<400> 18
tccactgacc ttgttgaca aattgccg 28

<210> 19
<211> 162
<212> PRT
<213> Alcaligenes sp.

<220>
<223> Alcaligenes sp. CrtZ Amino Acid

<400> 19
Met Thr Gln Phe Leu Ile Val Val Ala Thr Val Leu Val Met Glu Leu
1 5 10 15

Thr Ala Tyr Ser Val His Arg Trp Ile Met His Gly Pro Leu Gly Trp
20 25 30

Gly Trp His Lys Ser His His Glu Glu His Asp His Ala Leu Glu Lys
35 40 45

Asn Asp Leu Tyr Gly Val Val Phe Ala Val Leu Ala Thr Ile Leu Phe
50 55 60

Thr Val Gly Ala Tyr Trp Trp Pro Val Leu Trp Trp Ile Ala Leu Gly
65 70 75 80

Met Thr Val Tyr Gly Leu Ile Tyr Phe Ile Leu His Asp Gly Leu Val
85 90 95

His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Arg Gly Tyr Phe Arg
100 105 110

SubstCRFsequencelisting_2009Jul30.txt

Arg Leu Tyr Gln Ala His His Arg Leu His His Ala Val Glu Gly Arg Asp
115 120 125

His Cys Val Ser Phe Gly Phe Ile Tyr Ala Pro Pro Val Asp Lys Leu
130 135 140

Lys Gln Asp Leu Lys Arg Ser Gly Val Leu Arg Pro Gln Asp Glu Arg
145 150 155 160

Pro Ser

<210> 20

<211> 242

<212> PRT

<213> Alcaligenes sp.

<220>

<223> Alcaligenes sp. CrtW Amino Acid

<400> 20

Met Ser Gly Arg Lys Pro Gly Thr Thr Gly Asp Thr Ile Val Asn Leu
1 5 10 15

Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
20 25 30

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
35 40 45

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
100 105 110

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
115 120 125

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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SubstCRFsequencelisting_2009Jul30.txt

210

215

220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
 225 230 235 240

Arg Ala

<210> 21

<211> 258

<212> PRT

<213> Bradyrhizobium sp.

<220>

<223> Bradyrhizobium sp. CrtW Amino Acid

<400> 21

Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
 1 5 10 15

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
 20 25 30

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
 35 40 45

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
 50 55 60

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
 65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
 85 90 95

Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
 115 120 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
 130 135 140

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
 145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
 165 170 175

Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
 180 185 190

Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
 195 200 205

Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

SubstCRFsequencelisting_2009Jul30.txt
Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
245 250 255

Arg Asp

<210> 22
<211> 295
<212> PRT
<213> Flavobacterium sp.

<220>
<223> Flavobacterium sp. CrtE Amino Acid

<400> 22
Met Thr Pro Lys Gln Gln Phe Pro Leu Arg Asp Leu Val Glu Ile Arg
1 5 10 15

Leu Ala Gln Ile Ser Gly Gln Phe Gly Val Val Ser Ala Pro Leu Gly
20 25 30

Ala Ala Met Ser Asp Ala Ala Leu Ser Pro Gly Lys Arg Phe Arg Ala
35 40 45

Val Leu Met Leu Met Val Ala Glu Ser Ser Gly Gly Val Cys Asp Ala
50 55 60

Met Val Asp Ala Ala Cys Ala Val Glu Met Val His Ala Ala Ser Leu
65 70 75 80

Ile Phe Asp Asp Met Pro Cys Met Asp Asp Ala Arg Thr Arg Arg Gly
85 90 95

Gln Pro Ala Thr His Val Ala His Gly Glu Gly Arg Ala Val Leu Ala
100 105 110

Gly Ile Ala Leu Ile Thr Glu Ala Met Arg Ile Leu Gly Glu Ala Arg
115 120 125

Gly Ala Thr Pro Asp Gln Arg Ala Arg Leu Val Ala Ser Met Ser Arg
130 135 140

Ala Met Gly Pro Val Gly Leu Cys Ala Gly Gln Asp Leu Asp Leu His
145 150 155 160

Ala Pro Lys Asp Ala Ala Gly Ile Glu Arg Glu Gln Asp Leu Lys Thr
165 170 175

Gly Val Leu Phe Val Ala Gly Leu Glu Met Leu Ser Ile Ile Lys Gly
180 185 190

Leu Asp Lys Ala Glu Thr Glu Gln Leu Met Ala Phe Gly Arg Gln Leu
195 200 205

Gly Arg Val Phe Gln Ser Tyr Asp Asp Leu Leu Asp Val Ile Gly Asp
210 215 220

Lys Ala Ser Thr Gly Lys Asp Thr Ala Arg Asp Thr Ala Ala Pro Gly
225 230 235 240

Pro Lys Gly Gly Leu Met Ala Val Gly Gln Met Gly Asp Val Ala Gln

SubstCRFsequencelisting_2009Jul30.txt

245

250

255

His Tyr Arg Ala Ser Arg Ala Gln Leu Asp Glu Leu Met Arg Thr Arg
 260 265 270

Leu Phe Arg Gly Gly Gln Ile Ala Asp Leu Leu Ala Arg Val Leu Pro
 275 280 285

His Asp Ile Arg Arg Ser Ala
 290 295

<210> 23

<211> 303

<212> PRT

<213> Flavobacterium sp.

<220>
<223> Flavobacterium sp. CrtB Amino Acid<400> 23
Met Thr Asp Leu Thr Ala Thr Ser Glu Ala Ala Ile Ala Gln Gly Ser
 1 5 10 15Gln Ser Phe Ala Gln Ala Ala Lys Leu Met Pro Pro Gly Ile Arg Glu
 20 25 30Asp Thr Val Met Leu Tyr Ala Trp Cys Arg His Ala Asp Asp Val Ile
 35 40 45Asp Gly Gln Val Met Gly Ser Ala Pro Glu Ala Gly Gly Asp Pro Gln
 50 55 60Ala Arg Leu Gly Ala Leu Arg Ala Asp Thr Leu Ala Ala Leu His Glu
 65 70 75 80Asp Gly Pro Met Ser Pro Pro Phe Ala Ala Leu Arg Gln Val Ala Arg
 85 90 95Arg His Asp Phe Pro Asp Leu Trp Pro Met Asp Leu Ile Glu Gly Phe
 100 105 110Ala Met Asp Val Ala Asp Arg Glu Tyr Arg Ser Leu Asp Asp Val Leu
 115 120 125Glu Tyr Ser Tyr His Val Ala Gly Val Val Gly Val Met Met Ala Arg
 130 135 140Val Met Gly Val Gln Asp Asp Ala Val Leu Asp Arg Ala Cys Asp Leu
 145 150 155 160Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp Val Ile Asp Asp
 165 170 175Ala Ala Ile Gly Arg Cys Tyr Leu Pro Ala Asp Trp Leu Ala Glu Ala
 180 185 190Gly Ala Thr Val Glu Gly Pro Val Pro Ser Asp Ala Leu Tyr Ser Val
 195 200 205Ile Ile Arg Leu Leu Asp Ala Ala Glu Pro Tyr Tyr Ala Ser Ala Arg
 210 215 220

SubstCRFsequencelisting_2009Jul30.txt

Gln Gly Leu Pro His Leu Pro Pro Arg Cys Ala Trp Ser Ile Ala Ala
225 230 235 240
Ala Leu Arg Ile Tyr Arg Ala Ile Gly Thr Arg Ile Arg Gln Gly Gly
245 250 255
Pro Glu Ala Tyr Arg Gln Arg Ile Ser Thr Ser Lys Ala Ala Lys Ile
260 265 270
Gly Leu Leu Ala Arg Gly Gly Leu Asp Ala Ala Ser Arg Leu Arg
275 280 285
Gly Gly Glu Ile Ser Arg Asp Gly Leu Trp Thr Arg Pro Arg Ala
290 295 300

<210> 24
<211> 494
<212> PRT
<213> Flavobacterium sp.

<220>
<223> Flavobacterium sp. CrtI Amino Acid

<400> 24
Met Ser Ser Ala Ile Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
1 5 10 15
Ala Ile Arg Leu Gln Ser Ala Gly Ile Ala Thr Thr Ile Val Glu Ala
20 25 30
Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Trp Asn Asp Gln Gly His
35 40 45
Val Phe Asp Ala Gly Pro Thr Val Val Thr Asp Pro Asp Ser Leu Arg
50 55 60
Glu Leu Trp Ala Leu Ser Gly Gln Pro Met Glu Arg Asp Val Thr Leu
65 70 75 80
Leu Pro Val Ser Pro Phe Tyr Arg Leu Thr Trp Ala Asp Gly Arg Ser
85 90 95
Phe Glu Tyr Val Asn Asp Asp Asp Glu Leu Ile Arg Gln Val Ala Ser
100 105 110
Phe Asn Pro Ala Asp Val Asp Gly Tyr Arg Arg Phe His Asp Tyr Ala
115 120 125
Glu Glu Val Tyr Arg Glu Gly Tyr Leu Lys Leu Gly Thr Thr Pro Phe
130 135 140
Leu Lys Leu Gly Gln Met Leu Asn Ala Ala Pro Ala Leu Met Arg Leu
145 150 155 160
Gln Ala Tyr Arg Ser Val His Ser Met Val Ala Arg Phe Ile Gln Asp
165 170 175
Pro His Leu Arg Gln Ala Phe Ser Phe His Thr Leu Leu Val Gly Gly
180 185 190

SubstCRFsequencelisting_2009Jul30.txt

Asn Pro Phe Ser Thr Ser Ser Ile Tyr Ala Leu Ile His Ala Leu Glu
195 200 205

Arg Arg Gly Gly Val Trp Phe Ala Lys Gly Gly Thr Asn Gln Leu Val
210 215 220

Ala Gly Met Val Ala Leu Phe Glu Arg Leu Gly Gly Thr Leu Leu Leu
225 230 235 240

Asn Ala Arg Val Thr Arg Ile Asp Thr Glu Gly Asp Arg Ala Thr Gly
245 250 255

Val Thr Leu Leu Asp Gly Arg Gln Leu Arg Ala Asp Thr Val Ala Ser
260 265 270

Asn Gly Asp Val Met His Ser Tyr Arg Asp Leu Leu Gly His Thr Arg
275 280 285

Arg Gly Arg Thr Lys Ala Ala Ile Leu Asn Arg Gln Arg Trp Ser Met
290 295 300

Ser Leu Phe Val Leu His Phe Gly Leu Ser Lys Arg Pro Glu Asn Leu
305 310 315 320

Ala His His Ser Val Ile Phe Gly Pro Arg Tyr Lys Gly Leu Val Asn
325 330 335

Glu Ile Phe Asn Gly Pro Arg Leu Pro Asp Asp Phe Ser Met Tyr Leu
340 345 350

His Ser Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Met Ser
355 360 365

Thr His Tyr Val Leu Ala Pro Val Pro His Leu Gly Arg Ala Asp Val
370 375 380

Asp Trp Glu Ala Glu Ala Pro Gly Tyr Ala Glu Arg Ile Phe Glu Glu
385 390 395 400

Leu Glu Arg Arg Ala Ile Pro Asp Leu Arg Lys His Leu Thr Val Ser
405 410 415

Arg Ile Phe Ser Pro Ala Asp Phe Ser Thr Glu Leu Ser Ala His His
420 425 430

Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
435 440 445

Arg Pro His Asn Arg Asp Arg Ala Ile Pro Asn Phe Tyr Ile Val Gly
450 455 460

Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Val Gly Ser Ala
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Lys Ala Thr Ala Gln Val Met Leu Ser Asp Leu Ala Val Ala
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SubstCRFsequencelisting_2009Jul30.txt

<220>
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<400> 25
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20 25 30
Leu Asp Ala Arg Ser Gly Pro Ser Asp Gln His Thr Trp Ser Cys His
35 40 45
Asp Thr Asp Leu Ser Pro Glu Trp Leu Ala Arg Leu Ser Pro Ile Arg
50 55 60
Arg Gly Glu Trp Thr Asp Gln Glu Val Ala Phe Pro Asp His Ser Arg
65 70 75 80
Arg Leu Thr Thr Gly Tyr Gly Ser Ile Glu Ala Gly Ala Leu Ile Gly
85 90 95
Leu Leu Gln Gly Val Asp Leu Arg Trp Asn Thr His Val Ala Thr Leu
100 105 110
Asp Asp Thr Gly Ala Thr Leu Thr Asp Gly Ser Arg Ile Glu Ala Ala
115 120 125
Cys Val Ile Asp Ala Arg Gly Ala Val Glu Thr Pro His Leu Thr Val
130 135 140
Gly Phe Gln Lys Phe Val Gly Val Glu Ile Glu Thr Asp Ala Pro His
145 150 155 160
Gly Val Glu Arg Pro Met Ile Met Asp Ala Thr Val Pro Gln Met Asp
165 170 175
Gly Tyr Arg Phe Ile Tyr Leu Leu Pro Phe Ser Pro Thr Arg Ile Leu
180 185 190
Ile Glu Asp Thr Arg Tyr Ser Asp Gly Gly Asp Leu Asp Asp Gly Ala
195 200 205
Leu Ala Gln Ala Ser Leu Asp Tyr Ala Ala Arg Arg Gly Trp Thr Gly
210 215 220
Gln Glu Met Arg Arg Glu Arg Gly Ile Leu Pro Ile Ala Leu Ala His
225 230 235 240
Asp Ala Ile Gly Phe Trp Arg Asp His Ala Gln Gly Ala Val Pro Val
245 250 255
Gly Leu Gly Ala Gly Leu Phe His Pro Val Thr Gly Tyr Ser Leu Pro
260 265 270
Tyr Ala Ala Gln Val Ala Asp Ala Ile Ala Ala Arg Asp Leu Thr Thr
275 280 285
Ala Ser Ala Arg Arg Ala Val Arg Gly Trp Ala Ile Asp Arg Ala Asp
290 295 300
Arg Asp Arg Phe Leu Arg Leu Leu Asn Arg Met Leu Phe Arg Gly Cys

SubstCRFsequencelisting_2009Jul30.txt

305	310	315	320
Pro Pro Asp Arg Arg Tyr Arg Leu Leu Gln Arg Phe Tyr Arg Leu Pro			
325	330	335	
Gln Pro Leu Ile Glu Arg Phe Tyr Ala Gly Arg Leu Thr Leu Ala Asp			
340	345	350	
Arg Leu Arg Ile Val Thr Gly Arg Pro Pro Ile Pro Leu Ser Gln Ala			
355	360	365	
Val Arg Cys Leu Pro Glu Arg Pro Leu Leu Gln Glu Arg Ala			
370	375	380	